

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/535,522

CRF Edit Date: 6/2/05
Edited by: [signature]

☐ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

☒ Corrected the SEQ ID NO. Sequence numbers edited were:

10

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☒ Deleted: ☒ invalid beginning/end-of-file text ; ☐ page numbers

☒ Inserted mandatory headings/numeric identifiers, specifically:

C2207 in seqs. 8, 10

☐ Moved responses to same line as heading/numeric identifier, specifically:

☐ Other:



PCT

RAW SEQUENCE LISTING

DATE: 06/02/2005

PATENT APPLICATION: US/10/535,522

TIME: 14:09:45

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06022005\J535522.raw

```

3 <110> APPLICANT: Steinkasserer, Alexander
5 <120> TITLE OF INVENTION: Use of Soluble Forms of CD83 and Nucleic Acids Encoding
6   them for the Treatment or Prevention of Diseases
W--> 7 <130> FILE REFERENCE: 032723woJH
W--> 8 <140> CURRENT APPLICATION NUMBER:
C--> 9 <141> CURRENT FILING DATE: 2005-05-18
W--> 10 <160> NUMBER OF SEQ ID: 12
11 <170> SOFTWARE: PatentIn Ver. 2.1
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 618
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
W--> 18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (1)..(615)
22 <400> SEQUENCE: 1
23 atg tgc cgc ggc ctc cag ctt ctg ctc ctg agc tgc gcc tac agc ctg   48
24 Met Ser Arg Gly Leu Gln Leu Leu Leu Ser Cys Ala Tyr Ser Leu
25   1           5           10           15
27 gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac   96
28 Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
29           20           25           30
31 ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc   144
32 Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
33           35           40           45
35 tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag   192
36 Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
37   50           55           60
39 gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt   240
40 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
41  65           70           75           80
43 tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac   288
44 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
45           85           90           95
47 act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg   336
48 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
49           100           105           110
51 gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga   384
52 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
53           115           120           125
56 tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag   432
57 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
58   130           135           140

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60 att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att 480
61 Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
62 145 150 155 160
64 ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct 528
65 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
66 165 170 175
68 aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag 576
69 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
70 180 185 190
72 cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga 618
73 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
74 195 200 205
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 205
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 2
83 Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
84 1 5 10 15
86 Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
87 20 25 30
89 Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
90 35 40 45
92 Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
93 50 55 60
95 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
96 65 70 75 80
98 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
99 85 90 95
101 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
102 100 105 110
104 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
105 115 120 125
107 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
108 130 135 140
111 Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
112 145 150 155 160
114 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
115 165 170 175
117 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
118 180 185 190
120 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
121 195 200 205
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 2051
126 <212> TYPE: DNA
127 <213> ORGANISM: Mus musculus
W--> 128 <220> FEATURE:
129 <221> NAME/KEY: CDS

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06022005\J535522.raw

130 <222> LOCATION: (14)..(601)

132 <400> SEQUENCE: 3

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133 gcgctccagc cgc atg tcg caa ggc ctc cag ctc ctg ttt cta ggc tgc      49
134           Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys
135           1           5           10
137 gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct      97
138 Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
139           15           20           25
141 tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag      145
142 Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
143           30           35           40
145 ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag      193
146 Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
147           45           50           55           60
149 agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc      241
150 Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
151           65           70           75
153 agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc      289
154 Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
155           80           85           90
157 tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac      337
158 Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
159           95           100           105
161 ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct      385
162 Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
163           110           115           120
165 aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc      433
166 Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
167           125           130           135           140
169 tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt      481
170 Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
171           145           150           155
173 gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa      529
174 Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
175           160           165           170
177 caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg      577
178 Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
179           175           180           185
183 acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttacaag      631
184 Thr Leu Pro Lys Thr Glu Thr Val
185           190           195
187 ccaagggcac atcagatcag tgtgcctgaa tgccaccggg acaagagaag aatgagctcc      691
189 atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc      751
191 cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct      811
193 ctgtggctgt cagcttaatg tttcatgttg ctatctggtc aacctcgtga gtgcttttca      871
195 gtcattctaca agctatgggt agatgcaggt gaagcagggt catgggaaat ttgaacactc      931
197 tgagctggcc ctgtgacaga ctctgagga cagctgtcct ctctacatc tgggatacat      991
199 ctctttgaat ttgtcctgtt tcgttgacc agcccagatg tctcacatct ggcggaaatt      1051
201 gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt      1111

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06022005\J535522.raw

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203 cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagt aactattccc 1171
205 cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca 1231
207 catttatttt tttaatcttc atgtacttgt caaagaagaa tttttcatgt tttttcaaag 1291
209 aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga 1351
211 caagcagcct gagagaagat ggagaatgtt cttcaaaata gggacagcaa gctagaagca 1411
213 ctgtacagtg ccctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471
215 aagattgtct gtatgattct ggacgagtca cttgtggttt tcaactctctg gttagtaaac 1531
217 cagatagttt agtctggggt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg 1591
219 tagtgaatac attggcaact ctactgggct gttaccttgt tgatataccta gagttctgga 1651
221 gctgagcgaa tgctgtcat atctcagctt gcccatcaat ccaaacacag gaggtacaa 1711
223 aaaggacatg agcatggctt tctgtgtgaa ctctcctga gaaacgtgga gactggctca 1771
225 gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggacctg ggggagctat 1831
227 tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt 1891
229 taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgtccca ctaatggtgt 1951
231 gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011
233 tcagccatga ctttcatgct attaaaagaa tgcattgtgaa 2051
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 196
238 <212> TYPE: PRT
239 <213> ORGANISM: Mus musculus
241 <400> SEQUENCE: 4
242 Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys Ala Cys Ser Leu
243 1 5 10 15
245 Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala Cys Ser Glu Thr
246 20 25 30
248 Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
249 35 40 45
251 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
252 50 55 60
254 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
255 65 70 75 80
257 Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
258 85 90 95
260 Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
261 100 105 110
263 Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
264 115 120 125
266 Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
267 130 135 140
269 Phe Tyr Leu Thr Leu Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
270 145 150 155 160
272 Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
273 165 170 175
275 Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
276 180 185 190
278 Thr Glu Thr Val
279 195
282 <210> SEQ ID NO: 5
283 <211> LENGTH: 31

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RAW SEQUENCE LISTING

DATE: 06/02/2005

PATENT APPLICATION: US/10/535,522

TIME: 14:09:45

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06022005\J535522.raw

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284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
W--> 286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for CD83ext
289 <400> SEQUENCE: 5
290 tcccccgga acgccggagg tgaaggtggc t 31
293 <210> SEQ ID NO: 6
294 <211> LENGTH: 31
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
W--> 297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for CD83ext
300 <400> SEQUENCE: 6
301 aattagaatt ctcaaatctc cgctctgtat t 31
304 <210> SEQ ID NO: 7
305 <211> LENGTH: 435
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
W--> 308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: partial
310 sequence of pGEX2ThCD83ext
W--> 311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (1)..(417)
W--> 314 <220> FEATURE:
315 <221> NAME/KEY: mat_peptide
316 <222> LOCATION: (28)..(417)
318 <400> SEQUENCE: 7
319 cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag 48
320 Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
321 -5 -1 1 5
323 gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
324 Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
325 10 15 20
327 tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
328 Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
329 25 30 35
331 ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
332 Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
333 40 45 50 55
335 cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
336 Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
337 60 65 70
339 gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
340 Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
341 75 80 85
343 ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
344 Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
345 90 95 100

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VERIFICATION SUMMARY

DATE: 06/02/2005

PATENT APPLICATION: US/10/535,522

TIME: 14:09:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06022005\J535522.raw

L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:283 W: Missing Blank Line separator, <140> field identifier
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:283 W: Missing Blank Line separator, <160> field identifier
L:18 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <220> field identifier
L:286 M:283 W: Missing Blank Line separator, <220> field identifier
L:297 M:283 W: Missing Blank Line separator, <220> field identifier
L:308 M:283 W: Missing Blank Line separator, <220> field identifier
L:311 M:283 W: Missing Blank Line separator, <220> field identifier
L:314 M:283 W: Missing Blank Line separator, <220> field identifier
L:398 M:283 W: Missing Blank Line separator, <220> field identifier
L:401 M:283 W: Missing Blank Line separator, <220> field identifier
L:404 M:283 W: Missing Blank Line separator, <220> field identifier
L:450 M:283 W: Missing Blank Line separator, <220> field identifier
L:489 M:283 W: Missing Blank Line separator, <220> field identifier
L:501 M:283 W: Missing Blank Line separator, <220> field identifier